

# SEQUENCE LISTING

<110> Gerritsen, Mary  
Sliwkowski, Mark X.

<120> ErbB4 ANTAGONISTS

<130> GENENT.072A2

<150> 60/229,679

<151> 2000-09-01

<150> 60/265,516

<151> 2001-01-31

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 5484

<212> DNA

<213> Homo sapiens

<400> 1

aattgtcagc	acgggatctg	agacttccaa	aaaatgaagc	cggcgacagg	actttgggtc	60
tgggtgagcc	ttctcgtggc	ggcggggacc	gtccagccca	gcgattctca	gtcagtgtgt	120
gcaggaacgg	agaataaaact	gagctctctc	tctgacctgg	aacagcagta	ccgagccttg	180
cgcaagtact	atgaaaaactg	tgaggttgtc	atgggcaacc	tggagataac	cagcattgag	240
cacaaccggg	acctctcctt	cctgcggtct	gttcgagaag	tcacaggcta	cgtgttagtg	300
gctcttaaatc	agtttcgtta	cctgcctctg	gagaatttac	gcattattcg	tgggacaaaa	360
ctttatgagg	atcgatatgc	cttggcaata	tttttaaact	acagaaaaga	tggaaacttt	420
ggacttcaag	aacttggatt	aaagaacttg	acagaaatcc	taaatgggtg	agtctatgta	480
gaccagaaca	aattcctttg	ttatgcagac	accattcatt	ggcaagatat	tgttcggaac	540
ccatggcctt	ccaacttgac	tcttgtgtca	acaaatggta	gttcaggatg	tggacgttgc	600
cataagtcct	gtactggccg	ttgctgggga	cccacagaaa	atcattgcc	gactttgaca	660
aggacggtgt	gtgcagaaca	atgtgacggc	agatgctacg	gaccttacgt	cagtgactgc	720
tgccatcgag	aatgtgctgg	aggctgctca	ggacctaaag	acacagactg	ctttgcctgc	780
atgaatttca	atgacagtgg	agcatgtgtt	actcagtgtc	cccaaactct	tgtctacaat	840
ccaaccacct	ttcaactgga	gcacaatttc	aatgcaaagt	acacatatgg	agcattctgt	900
gtcaagaaat	gtccacataa	ctttgtggta	gattccagtt	cttgtgtgcg	tgcctgccct	960
agttccaaga	tggaagtaga	agaaaatggg	attaaaatgt	gtaaaccttg	cactgacatt	1020
tgcccaaaag	cttgtgatgg	cattggcaca	ggatcattga	tgtcagctca	gactgtggat	1080
tccagtaaca	ttgacaaatt	cataaactgt	accaagatca	atgggaattt	gatctttcta	1140
gtcactggta	ttcatgggga	cccttacaat	gcaattgaag	ccatagaccc	agagaaaactg	1200
aacgtctttc	ggacagtcag	agagataaca	ggtttcctga	acatacagtc	atggccacca	1260
aacatgactg	acttcagtgt	tttttctaac	ctggtgacca	ttggtggaag	agtactctat	1320
agtggcctgt	ccttgcttat	cctcaagcaa	cagggcatca	cctctctaca	gttccagtcc	1380
ctgaaggaaa	tcagcgcagg	aaacatctat	attactgaca	acagcaacct	gtgttattat	1440
cataccatta	actggacaac	actcttcagc	acaatcaacc	agagaatagt	aatccgggac	1500
aacagaaaag	ctgaaaaattg	tactgctgaa	ggaatgggtg	gcaaccatct	gtgttcagct	1560
gatggctgtt	ggggacctgg	gccagaccaa	tgtctgtcgt	gtcgccgctt	cagtagagga	1620
aggatctgca	tagagtcttg	taacctctat	gatggtgaat	ttcgggagtt	tgagaatggc	1680
tccatctgtg	tggagtgtga	cccccagtgt	gagaagatgg	aagatggcct	cctcacatgc	1740
catggaccgg	gtcctgacaa	ctgtacaaag	tgctctcatt	ttaaagatgg	cccaaactgt	1800

09940101.082701

gtggaaaaat	gtccagatgg	cttacagggg	gcaaacagtt	tcattttcaa	gtatgctgat	1860
ccagatcggg	agtgccaccc	atgccatcca	aactgcaccc	aaggggtgtaa	cggtccact	1920
agtcattgact	gcattttacta	cccatggacg	ggccattcca	ctttaccaca	acatgctaga	1980
actcccctga	ttgcagctgg	agtaattggg	gggctcttca	ttctgggcat	tgtgggtctg	2040
acatttgctg	tttatgttag	aaggaagagc	atcaaaaaga	aaagagcctt	gagaagattc	2100
ttggaaacag	agttgggtgga	accattaact	cccagtgcca	cagcacccaa	tcaagctcaa	2160
cttcgtat	tgaaagaaac	tgagctgaag	agggtaaaag	tccttggtctc	aggtgctttt	2220
ggaacggttt	ataaaggtat	ttgggtacct	gaaggagaaa	ctgtgaagat	tcctgtggct	2280
attaagattc	ttaatgagac	aactgggtccc	aaggcaaagt	tggagtccat	ggatgaagct	2340
ctgatcatgg	caagtatgga	tcattccacac	ctagtccggg	tgctgggtgt	gtgtctgagc	2400
ccaaccatcc	agctgggttac	tcaacttatg	ccccatggct	gcctgttgga	gtatgtccac	2460
gagcacaagg	ataacattgg	atcacaaactg	ctgtcttaact	ggtgtgtcca	gatagctaag	2520
ggaatgatgt	acctggaaga	aagacgactc	gttcatcggt	atttggcagc	ccgtaattgc	2580
ttagtgaat	ctccaaacca	tgtgaaaatc	acagattttg	ggctagccag	actcttggaa	2640
ggagatgaaa	aagagtacaa	tgctgatgga	ggaaagatgc	caattaaatg	gatggctctg	2700
gagtgtatac	attacaggaa	attcacccat	cagagtgcag	tttggagcta	tggagtact	2760
atatgggaac	tgatgacctt	tggaggaaaa	ccctatgatg	gaattccaac	gcgagaaatc	2820
cctgattttat	tagagaaagg	agaacgtttg	cctcagcctc	ccatctgcac	tattgacgtt	2880
tacatggtca	tgggtcaaagt	ttggatgatt	gatgctgaca	gtagacctaa	atttaaggaa	2940
ctggctgctg	agttttcaag	gatggctcga	gacctcaaaa	gatacctagt	tattcagggg	3000
gatgatcgta	tgaagcttcc	cagtccaaat	gacagcaagt	tctttcagaa	tctcttggat	3060
gaagaggatt	tggaaagatat	gatggatgct	gaggagtact	tgggtccctca	ggctttcaac	3120
atcccacctc	ccatctatac	ttccagagca	agaattgact	cgaataggag	tgaattgga	3180
cacagccctc	ctcctgccta	cacccccatg	tcaggaaaacc	agtttgtata	ccgagatgga	3240
ggttttgctg	ctgaacaagg	agtgtctgtg	ccctacagag	ccccaaactag	cacaattcca	3300
gaagctcctg	tggcacaggg	tgctactgct	gagatttttg	atgactcctg	ctgtaatggc	3360
accctacgca	agccagtggc	acccccatgtc	caagaggaca	gtagcaccca	gaggtacagt	3420
gctgacccca	ccgtgtttgc	cccagaacgg	agcccacgag	gagagctgga	tgagggaagg	3480
tacatgactc	ctatgcgaga	caaaccctaaa	caagaatacc	tgaatccagt	ggaggagaac	3540
ccttttggtt	ctcggagaaa	aaatggagac	cttcaagcat	tggataatcc	cgaatatcac	3600
aatgcatcca	atgggtccacc	caaggccgag	gatgagtatg	tgaatgagcc	actgtacctc	3660
aacacctttg	ccaacacett	gggaaaagct	gagtacctga	agaacaacat	actgtcaatg	3720
ccagagaagg	ccaagaaagc	gtttgacaac	cctgactact	ggaaccacag	cctgccacct	3780
cggagcaccc	ttcagcaccc	agactacctg	caggagtaca	gcacaaaata	tttttataaa	3840
cagaatgggc	ggatccggcc	tattgtggca	gagaatcctg	aatacctctc	tgagttctcc	3900
ctgaagccag	gcaactgtgt	gccgcctcca	ccttacagac	accggaatac	tgtgggtgtaa	3960
gctcagttgt	ggttttttag	gtggagagac	acacctgctc	caatttcccc	acccccctct	4020
ctttctctgg	tgggtcttct	tctaccccaa	ggccagtagt	tttgacactt	cccagtgga	4080
gatacagaga	tgcaatgata	gttatgtgtc	tacctaaact	gaacattaga	gggaaagact	4140
gaaagagaaa	gataggagga	accacaatgt	ttcttcattt	ctctgcatgg	gttgggtcagg	4200
agaatgaaac	agctagagaa	ggaccagaaa	atgtaaggca	atgctgccta	ctatcaaaact	4260
agctgtcact	ttttttcttt	ttctttttct	ttctttgttt	ctttcttcct	cttctttttt	4320
tttttttttt	taaagcagat	ggttgaaaca	cccatgctat	ctgttcctat	ctgcaggaac	4380
tgatgtgtgc	atatttagca	tccctggaaa	tcataataaa	gtttccatta	gaacaaaaga	4440
ataacatttt	ctataacata	tgatagtgtc	tgaatttgag	aatccagttt	ctttccccag	4500
cagtttctgt	cctagcaagt	agaatggcc	aactcaactt	tcataattta	aaaatctcca	4560
ttaaagttat	aactagtaat	tatgttttca	acactttttg	gtttttttca	ttttgttttg	4620
ctctgaccga	ttcctttata	tttgcctccc	tatttttggc	tttaatttct	aattgcaaag	4680
atgtttacat	caaagcttct	tcacagaatt	taagcaagaa	atattttaat	atagtgaat	4740
ggccactact	ttaagtatac	aatctttaa	ataagaaagg	gaggctaata	ttttcatagc	4800
tatcaaat	tcttcaccct	catcctttac	atttttcaac	attttttttt	ctccataaat	4860
gacactactt	gagtagccgt	tgggtgtctg	aagagttagaa	gggaaactaa	gagacagttc	4920
tctgtggttc	aggaaaacta	ctgatacttt	caggggtggc	ccaatgaggg	aatccattga	4980
actggaagaa	acacactgga	ttgggtatgt	ctacctggca	gatactcaga	aatgtagttt	5040
gcacttaagc	tgtaatttta	tttgttcttt	ttctgaactc	catttttgat	tttgaatcaa	5100
gcaatatgga	agcaaccagc	aaattaacta	attttaagtac	atttttaaaa	aaagagctaa	5160
gataaagact	gtggaaatgc	caaaccaagc	aaattaggaa	ccttgcaacg	gtatccaggg	5220

actatgatga gaggccagca cattatcttc atatgtcacc ttgctacgc aaggaaattt 5280  
gttcagttcg tatacttcgt aagaaggaat gcgagtaagg attggcttga attccatgga 5340  
atttctagta tgagactatt tatatgaagt agaaggtaac tctttgcaca taaattggta 5400  
taataaaaag aaaaacacaa acattcaaag cttagggata ggtccttggg tcaaaagtgt 5460  
taaataaatg tgaaacatct tctc 5484

<210> 2  
<211> 1308  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Lys Pro Ala Thr Gly Leu Trp Val Trp Val Ser Leu Leu Val Ala  
1 5 10 15  
Ala Gly Thr Val Gln Pro Ser Asp Ser Gln Ser Val Cys Ala Gly Thr  
20 25 30  
Glu Asn Lys Leu Ser Ser Leu Ser Asp Leu Glu Gln Gln Tyr Arg Ala  
35 40 45  
Leu Arg Lys Tyr Tyr Glu Asn Cys Glu Val Val Met Gly Asn Leu Glu  
50 55 60  
Ile Thr Ser Ile Glu His Asn Arg Asp Leu Ser Phe Leu Arg Ser Val  
65 70 75 80  
Arg Glu Val Thr Gly Tyr Val Leu Val Ala Leu Asn Gln Phe Arg Tyr  
85 90 95  
Leu Pro Leu Glu Asn Leu Arg Ile Ile Arg Gly Thr Lys Leu Tyr Glu  
100 105 110  
Asp Arg Tyr Ala Leu Ala Ile Phe Leu Asn Tyr Arg Lys Asp Gly Asn  
115 120 125  
Phe Gly Leu Gln Glu Leu Gly Leu Lys Asn Leu Thr Glu Ile Leu Asn  
130 135 140  
Gly Gly Val Tyr Val Asp Gln Asn Lys Phe Leu Cys Tyr Ala Asp Thr  
145 150 155 160  
Ile His Trp Gln Asp Ile Val Arg Asn Pro Trp Pro Ser Asn Leu Thr  
165 170 175  
Leu Val Ser Thr Asn Gly Ser Ser Gly Cys Gly Arg Cys His Lys Ser  
180 185 190  
Cys Thr Gly Arg Cys Trp Gly Pro Thr Glu Asn His Cys Gln Thr Leu  
195 200 205  
Thr Arg Thr Val Cys Ala Glu Gln Cys Asp Gly Arg Cys Tyr Gly Pro  
210 215 220  
Tyr Val Ser Asp Cys Cys His Arg Glu Cys Ala Gly Gly Cys Ser Gly  
225 230 235 240  
Pro Lys Asp Thr Asp Cys Phe Ala Cys Met Asn Phe Asn Asp Ser Gly  
245 250 255  
Ala Cys Val Thr Gln Cys Pro Gln Thr Phe Val Tyr Asn Pro Thr Thr  
260 265 270  
Phe Gln Leu Glu His Asn Phe Asn Ala Lys Tyr Thr Tyr Gly Ala Phe  
275 280 285  
Cys Val Lys Lys Cys Pro His Asn Phe Val Val Asp Ser Ser Ser Cys  
290 295 300  
Val Arg Ala Cys Pro Ser Lys Met Glu Val Glu Glu Asn Gly Ile  
305 310 315 320  
Lys Met Cys Lys Pro Cys Thr Asp Ile Cys Pro Lys Ala Cys Asp Gly  
325 330 335  
Ile Gly Thr Gly Ser Leu Met Ser Ala Gln Thr Val Asp Ser Ser Asn  
340 345 350  
Ile Asp Lys Phe Ile Asn Cys Thr Lys Ile Asn Gly Asn Leu Ile Phe

00940101.DB2701

09940101-082701  
T02280-T040660

355	360	365
Leu Val Thr Gly Ile His	Gly Asp Pro Tyr Asn	Ala Ile Glu Ala Ile
370	375	380
Asp Pro Glu Lys Leu Asn	Val Phe Arg Thr Val	Arg Glu Ile Thr Gly
385	390	395
Phe Leu Asn Ile Gln Ser	Trp Pro Pro Asn Met	Thr Asp Phe Ser Val
405	410	415
Phe Ser Asn Leu Val Thr	Ile Gly Gly Arg Val	Leu Tyr Ser Gly Leu
420	425	430
Ser Leu Leu Ile Leu Lys	Gln Gln Gly Ile Thr	Ser Leu Gln Phe Gln
435	440	445
Ser Leu Lys Glu Ile Ser	Ala Gly Asn Ile Tyr	Ile Thr Asp Asn Ser
450	455	460
Asn Leu Cys Tyr Tyr His	Thr Ile Asn Trp Thr	Thr Leu Phe Ser Thr
465	470	475
Ile Asn Gln Arg Ile Val	Ile Arg Asp Asn Arg	Lys Ala Glu Asn Cys
485	490	495
Thr Ala Glu Gly Met Val	Cys Asn His Leu Cys	Ser Ser Asp Gly Cys
500	505	510
Trp Gly Pro Gly Pro Asp	Gln Cys Leu Ser Cys	Arg Arg Phe Ser Arg
515	520	525
Gly Arg Ile Cys Ile Glu	Ser Cys Asn Leu Tyr	Asp Gly Glu Phe Arg
530	535	540
Glu Phe Glu Asn Gly Ser	Ile Cys Val Glu Cys	Asp Pro Gln Cys Glu
545	550	555
Lys Met Glu Asp Gly Leu	Leu Thr Cys His Gly	Pro Gly Pro Asp Asn
565	570	575
Cys Thr Lys Cys Ser His	Phe Lys Asp Gly Pro	Asn Cys Val Glu Lys
580	585	590
Cys Pro Asp Gly Leu Gln	Gly Ala Asn Ser Phe	Ile Phe Lys Tyr Ala
595	600	605
Asp Pro Asp Arg Glu Cys	His Pro Cys His Pro	Asn Cys Thr Gln Gly
610	615	620
Cys Asn Gly Pro Thr Ser	His Asp Cys Ile Tyr	Tyr Pro Trp Thr Gly
625	630	635
His Ser Thr Leu Pro Gln	His Ala Arg Thr Pro	Leu Ile Ala Ala Gly
645	650	655
Val Ile Gly Gly Leu Phe	Ile Leu Val Ile Val	Gly Leu Thr Phe Ala
660	665	670
Val Tyr Val Arg Arg Lys	Ser Ile Lys Lys Lys	Arg Ala Leu Arg Arg
675	680	685
Phe Leu Glu Thr Glu Leu	Val Glu Pro Leu Thr	Pro Ser Gly Thr Ala
690	695	700
Pro Asn Gln Ala Gln Leu	Arg Ile Leu Lys Glu	Thr Glu Leu Lys Arg
705	710	715
Val Lys Val Leu Gly Ser	Gly Ala Phe Gly Thr	Val Tyr Lys Gly Ile
725	730	735
Trp Val Pro Glu Gly Glu	Thr Val Lys Ile Pro	Val Ala Ile Lys Ile
740	745	750
Leu Asn Glu Thr Thr Gly	Pro Lys Ala Asn Val	Glu Phe Met Asp Glu
755	760	765
Ala Leu Ile Met Ala Ser	Met Asp His Pro His	Leu Val Arg Leu Leu
770	775	780
Gly Val Cys Leu Ser Pro	Thr Ile Gln Leu Val	Thr Gln Leu Met Pro
785	790	795
His Gly Cys Leu Leu Glu	Tyr Val His Glu His	Lys Asp Asn Ile Gly
805	810	815

09540101.032701

Ser	Gln	Leu	Leu	Leu	Asn	Trp	Cys	Val	Gln	Ile	Ala	Lys	Gly	Met	Met		
			820					825					830				
Tyr	Leu	Glu	Glu	Arg	Arg	Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn		
		835					840					845					
Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	Ile	Thr	Asp	Phe	Gly	Leu		
		850				855					860						
Ala	Arg	Leu	Leu	Glu	Gly	Asp	Glu	Lys	Glu	Tyr	Asn	Ala	Asp	Gly	Gly		
865					870					875					880		
Lys	Met	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Cys	Ile	His	Tyr	Arg	Lys		
				885					890						895		
Phe	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Ile	Trp	Glu		
			900					905									
Leu	Met	Thr	Phe	Gly	Gly	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Thr	Arg	Glu		
		915					920					925					
Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro	Gln	Pro	Pro	Ile		
		930				935					940						
Cys	Thr	Ile	Asp	Val	Tyr	Met	Val	Met	Val	Lys	Cys	Trp	Met	Ile	Asp		
945					950					955					960		
Ala	Asp	Ser	Arg	Pro	Lys	Phe	Lys	Glu	Leu	Ala	Ala	Glu	Phe	Ser	Arg		
				965				970							975		
Met	Ala	Arg	Asp	Pro	Gln	Arg	Tyr	Leu	Val	Ile	Gln	Gly	Asp	Asp	Arg		
			980					985					990				
Met	Lys	Leu	Pro	Ser	Pro	Asn	Asp	Ser	Lys	Phe	Phe	Gln	Asn	Leu	Leu		
		995				1000						1005					
Asp	Glu	Glu	Asp	Leu	Glu	Asp	Met	Met	Asp	Ala	Glu	Glu	Tyr	Leu	Val		
	1010					1015					1020						
Pro	Gln	Ala	Phe	Asn	Ile	Pro	Pro	Pro	Ile	Tyr	Thr	Ser	Arg	Ala	Arg		
1025					1030					1035					1040		
Ile	Asp	Ser	Asn	Arg	Ser	Glu	Ile	Gly	His	Ser	Pro	Pro	Pro	Ala	Tyr		
			1045						1050						1055		
Thr	Pro	Met	Ser	Gly	Asn	Gln	Phe	Val	Tyr	Arg	Asp	Gly	Gly	Phe	Ala		
			1060					1065							1070		
Ala	Glu	Gln	Gly	Val	Ser	Val	Pro	Tyr	Arg	Ala	Pro	Thr	Ser	Thr	Ile		
		1075					1080					1085					
Pro	Glu	Ala	Pro	Val	Ala	Gln	Gly	Ala	Thr	Ala	Glu	Ile	Phe	Asp	Asp		
	1090					1095					1100						
Ser	Cys	Cys	Asn	Gly	Thr	Leu	Arg	Lys	Pro	Val	Ala	Pro	His	Val	Gln		
1105				1110						1115					1120		
Glu	Asp	Ser	Ser	Thr	Gln	Arg	Tyr	Ser	Ala	Asp	Pro	Thr	Val	Phe	Ala		
				1125					1130						1135		
Pro	Glu	Arg	Ser	Pro	Arg	Gly	Glu	Leu	Asp	Glu	Glu	Gly	Tyr	Met	Thr		
			1140					1145					1150				
Pro	Met	Arg	Asp	Lys	Pro	Lys	Gln	Glu	Tyr	Leu	Asn	Pro	Val	Glu	Glu		
		1155					1160					1165					
Asn	Pro	Phe	Val	Ser	Arg	Arg	Lys	Asn	Gly	Asp	Leu	Gln	Ala	Leu	Asp		
	1170					1175					1180						
Asn	Pro	Glu	Tyr	His	Asn	Ala	Ser	Asn	Gly	Pro	Pro	Lys	Ala	Glu	Asp		
1185					1190					1195					1200		
Glu	Tyr	Val	Asn	Glu	Pro	Leu	Tyr	Leu	Asn	Thr	Phe	Ala	Asn	Thr	Leu		
			1205						1210						1215		
Gly	Lys	Ala	Glu	Tyr	Leu	Lys	Asn	Asn	Ile	Leu	Ser	Met	Pro	Glu	Lys		
			1220				1225						1230				
Ala	Lys	Lys	Ala	Phe	Asp	Asn	Pro	Asp	Tyr	Trp	Asn	His	Ser	Leu	Pro		
		1235					1240					1245					
Pro	Arg	Ser	Thr	Leu	Gln	His	Pro	Asp	Tyr	Leu	Gln	Glu	Tyr	Ser	Thr		
	1250					1255					1260						
Lys	Tyr	Phe	Tyr	Lys	Gln	Asn	Gly	Arg	Ile	Arg	Pro	Ile	Val	Ala	Glu		

1265		1270		1275		1280
Asn Pro Glu Tyr Leu Ser Glu Phe Ser Leu Lys Pro Gly Thr Val Leu						
		1285		1290		1295
Pro Pro Pro Pro Tyr Arg His Arg Asn Thr Val Val						
	1300		1305			

<210> 3  
 <211> 2601  
 <212> DNA  
 <213> Homo sapiens

<400> 3

ccaatcgatt	tcgcggcaaa	gaccttccgg	tcctggacca	gctgctcgag	cagtcagtgt	60
gtgcaggaac	ggagaataaa	ctgagctctc	tctctgacct	ggaacagcag	taccgagcct	120
tgcgcaagta	ctatgaaaac	tgtgaggttg	tcatgggcaa	cctggagata	accagcattg	180
agcacaaccg	ggacctctcc	ttcctgcggt	ctgttcgaga	agtcacaggc	tacgtgttag	240
tggctcttaa	tcagtttcgt	tacctgcctc	tggagaattt	acgcattatt	cgtgggacaa	300
aactttatga	ggatcgatat	gccttggcaa	tattttttaa	ctacagaaaa	gatggaaact	360
ttggacttca	agaacttgga	ttaaagaact	tgacagaaat	cctaaatggg	ggagtctatg	420
tagaccagaa	caaattcctt	tgttatgcag	acaccattca	ttggcaagat	attgttcgga	480
acccatggcc	ttccaacttg	actcttgtgt	caacaaatgg	tagttcagga	tgtggacggt	540
gccataagtc	ctgtactggc	cgttgctggg	gacccacaga	aaatcattgc	cagactttga	600
caaggacggt	gtgtgcagaa	caatgtgacg	gcagatgcta	cggaccttac	gtcagtgcact	660
gctgccatcg	agaatgtgct	ggaggctgct	caggacctaa	ggacacagac	tgctttgcct	720
gcatgaattt	caatgacagt	ggagcatgtg	ttactcagtg	tcccaaaacc	tttgtctaca	780
atccaaccac	ctttcaactg	gagcacaatt	tcaatgcaaa	gtacacatat	ggagcattct	840
gtgtcaagaa	atgtccacat	aactttgtgg	tagattccag	ttcttgtgtg	cgtgcctgcc	900
ctagttccaa	gatggaagta	gaagaaaatg	ggattaaaat	gtgtaaacct	tgactgaca	960
tttgcccaaa	agcttgtgat	ggcattggca	caggatcatt	gatgtcagct	cagactgtgg	1020
attccagtaa	cattgacaaa	ttcataaact	gtaccaagat	caatgggaat	ttgatctttc	1080
tagtcaactg	tattcatggg	gacccttaca	atgcaattga	agccatagac	ccagagaaac	1140
tgaacgtctt	tcggacagtc	agagagataa	caggtttcct	gaacatacag	tcattggccac	1200
caaacatgac	tgacttcagt	gttttttcta	acctggtgac	cattggtgga	agagtactct	1260
atagtggcct	gtccttgctt	atcctcaagc	aacagggcat	cacctctcta	cagttccagt	1320
ccctgaagga	aatcagcgca	ggaaacatct	atattactga	caacagcaac	ctgtgttatt	1380
atcataccat	taactggaca	acactcttca	gcacaatcaa	ccagagaata	gtaatccggg	1440
acaacagaaa	agctgaaaat	tgtactgctg	aaggaatggg	gtgcaaccat	ctgtgttcca	1500
gtgatggctg	ttggggacct	gggccagacc	aatgtctgtc	gtgtcgccgc	ttcagtagag	1560
gaaggatctg	catagagtct	tgtaacctct	atgatggtga	atttcgggag	tttgagaatg	1620
gtcccatctg	tgtggagtgt	gacccccagt	gtgagaagat	ggaagatggc	ctcctcacat	1680
gccatggacc	gggtcctgac	aactgtacaa	agtgtctctca	ttttaaagat	ggcccaaact	1740
gtgtggaaaa	atgtccagat	ggcttacagg	gggcaaacag	tttcattttc	aagtatgctg	1800
atccagatcg	ggagtgccac	ccatgccatc	caaactgcac	ccaagggtgt	aacggtccca	1860
ctagtcatga	ctgcatttac	tacctatgga	cgggcacgcg	tgacaaaact	cacacatgcc	1920
caccgtgccc	agcacctgaa	ctcctggggg	gaccgtcagt	cttcctcttc	ccccaaaac	1980
ccaaggacac	cctcatgate	tcccggaacc	ctgaggtcac	atgctgtgtg	gtggacgtga	2040
gccacgaaga	cctgaggtgc	aagttcaact	ggtacgtgga	cggcgtggag	gtgcataatg	2100
ccaagacaaa	gccgcgggag	gagcagtaca	acagcacgta	ccgggtggtc	agcgtcctca	2160
ccgtcctgca	ccaggactgg	ctgaatggca	aggagtacaa	gtgcaaggtc	tccaacaaag	2220
ccctccagc	cccatcgag	aaaaccactc	ccaaagccaa	agggcagccc	cgagaaccac	2280
agggtgtac	cctgccccca	tcccgggaag	agatgaccaa	gaaccaggtc	agcctgacct	2340
gctgtgtcaa	aggcttctat	cccagcgaca	tcgccgtgga	gtgggagagc	aatgggcagc	2400
cggagaacaa	ctggcccacc	cccttggttt	acaagaccac	gcctcccgtg	ctggactccg	2460
acggctcctt	cttcctctac	agcaagctca	ccgtggacaa	gagcaggtgg	cagcagggga	2520
acgtcttctc	atgctccgtg	atgcatgagg	ctctgcacaa	ccactacacg	cagaagagcc	2580
tctccctgtc	tccgggtaaa	t				2601

09940101-082701

<210> 4  
 <211> 615  
 <212> PRT  
 <213> Homo sapiens

<400> 4

Gln	Ser	Val	Cys	Ala	Gly	Thr	Glu	Asn	Lys	Leu	Ser	Ser	Leu	Ser	Asp
1				5					10					15	
Leu	Glu	Gln	Gln	Tyr	Arg	Ala	Leu	Arg	Lys	Tyr	Tyr	Glu	Asn	Cys	Glu
			20					25					30		
Val	Val	Met	Gly	Asn	Leu	Glu	Ile	Thr	Ser	Ile	Glu	His	Asn	Arg	Asp
		35					40					45			
Leu	Ser	Phe	Leu	Arg	Ser	Val	Arg	Glu	Val	Thr	Gly	Tyr	Val	Leu	Val
	50					55					60				
Ala	Leu	Asn	Gln	Phe	Arg	Tyr	Leu	Pro	Leu	Glu	Asn	Leu	Arg	Ile	Ile
65					70					75					80
Arg	Gly	Thr	Lys	Leu	Tyr	Glu	Asp	Arg	Tyr	Ala	Leu	Ala	Ile	Phe	Leu
			85						90					95	
Asn	Tyr	Arg	Lys	Asp	Gly	Asn	Phe	Gly	Leu	Gln	Glu	Leu	Gly	Leu	Lys
			100					105					110		
Asn	Leu	Thr	Glu	Ile	Leu	Asn	Gly	Gly	Val	Tyr	Val	Asp	Gln	Asn	Lys
		115					120					125			
Phe	Leu	Cys	Tyr	Ala	Asp	Thr	Ile	His	Trp	Gln	Asp	Ile	Val	Arg	Asn
	130					135					140				
Pro	Trp	Pro	Ser	Asn	Leu	Thr	Leu	Val	Ser	Thr	Asn	Gly	Ser	Ser	Gly
145					150					155					160
Cys	Gly	Arg	Cys	His	Lys	Ser	Cys	Thr	Gly	Arg	Cys	Trp	Gly	Pro	Thr
				165					170					175	
Glu	Asn	His	Cys	Gln	Thr	Leu	Thr	Arg	Thr	Val	Cys	Ala	Glu	Gln	Cys
			180					185					190		
Asp	Gly	Arg	Cys	Tyr	Gly	Pro	Tyr	Val	Ser	Asp	Cys	Cys	His	Arg	Glu
		195					200					205			
Cys	Ala	Gly	Gly	Cys	Ser	Gly	Pro	Lys	Asp	Thr	Asp	Cys	Phe	Ala	Cys
	210					215					220				
Met	Asn	Phe	Asn	Asp	Ser	Gly	Ala	Cys	Val	Thr	Gln	Cys	Pro	Gln	Thr
225					230					235					240
Phe	Val	Tyr	Asn	Pro	Thr	Thr	Phe	Gln	Leu	Glu	His	Asn	Phe	Asn	Ala
				245				250						255	
Lys	Tyr	Thr	Tyr	Gly	Ala	Phe	Cys	Val	Lys	Lys	Cys	Pro	His	Asn	Phe
			260					265					270		
Val	Val	Asp	Ser	Ser	Ser	Cys	Val	Arg	Ala	Cys	Pro	Ser	Ser	Lys	Met
		275					280					285			
Glu	Val	Glu	Glu	Asn	Gly	Ile	Lys	Met	Cys	Lys	Pro	Cys	Thr	Asp	Ile
	290					295					300				
Cys	Pro	Lys	Ala	Cys	Asp	Gly	Ile	Gly	Thr	Gly	Ser	Leu	Met	Ser	Ala
305					310					315					320
Gln	Thr	Val	Asp	Ser	Ser	Asn	Ile	Asp	Lys	Phe	Ile	Asn	Cys	Thr	Lys
				325					330					335	
Ile	Asn	Gly	Asn	Leu	Ile	Phe	Leu	Val	Thr	Gly	Ile	His	Gly	Asp	Pro
			340					345					350		
Tyr	Asn	Ala	Ile	Glu	Ala	Ile	Asp	Pro	Glu	Lys	Leu	Asn	Val	Phe	Arg
		355					360					365			
Thr	Val	Arg	Glu	Ile	Thr	Gly	Phe	Leu	Asn	Ile	Gln	Ser	Trp	Pro	Pro
	370					375					380				
Asn	Met	Thr	Asp	Phe	Ser	Val	Phe	Ser	Asn	Leu	Val	Thr	Ile	Gly	Gly
385					390					395					400

00940101-002701

